



SEQUENCE LISTING

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Trafuri Bladt, Anna
Senaldi, Giorgio

<120> Novel Polypeptides Involved in Immune Response

<130> 6843.0050-03

<140> 09/728,421

<141> 2000-11-28

<150> PCT/US00/01871

<151> 2000-01-27

<150> US 09/264,527

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<150> US 09/244,448

<151> 1999-02-03

<160> 37

<170> PatentIn version 3.1

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ctt tta aca gga gaa atc aat ggc tgc gcc gat cat agg atg ttt tca	96
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser	
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ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc	144
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val	
35 40 45	
cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa	192
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu	
50 55 60	
ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca	240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro	
65 70 75 80	
atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta	288
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
85 90 95	
aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc	336

Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser		
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Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr		
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ttg	cat	att	tat	gaa	tcc	cag	ctc	tgc	tgc	cag	ctg	aag	ctc	tgg	cta		432
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu		
	130					135					140						
ccc	gta	ggg	tgt	gca	gct	ttc	gtt	gtg	gta	ctc	ctt	ttt	gga	tgc	ata		480
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	Leu	Leu	Phe	Gly	Cys	Ile		
	145				150					155					160		
ctt	atc	atc	tgg	ttt	tca	aaa	aag	aaa	tac	gga	tcc	agt	gtg	cat	gac		528
Leu	Ile	Ile	Trp	Phe	Ser	Lys	Lys	Lys	Tyr	Gly	Ser	Ser	Val	His	Asp		
				165					170					175			
cct	aat	agt	gaa	tac	atg	ttc	atg	gcg	gca	gtc	aac	aca	aac	aaa	aag		576
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys		
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			20					25					30				
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val		
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Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu		
	50					55					60						
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Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu		
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115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
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35 40 45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
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Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
35 40 45

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
65 70 75 80

Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
85 90 95

Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
100 105 110

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
130 135 140

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
210 215

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<213> Artificial sequence

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Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu
20 25 30

Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala
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ggt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96
Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30
ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act 144
Leu Phe Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp 50 55 60	192
ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln 65 70 75 80	240
atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser 85 90 95	288
cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser 100 105 110	336
ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val 115 120 125	384
acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr 130 135 140	432
gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val 145 150 155 160	480
gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn 165 170 175	528
ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro 180 185 190	576
gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp 195 200 205	624
acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr 210 215 220	672
gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val 225 230 235 240	720
ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile 245 250 255	768
agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu 260 265 270	816
acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu 275 280 285	864
gcg gca gcg gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro 290 295 300	912

cac cga agc tat aca gga ccc aag act gta cag ctt gaa ctt aca gac 960
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cac gcc 966
His Ala

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Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
305 310 315 320

His Ala

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Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30

Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
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His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
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His Ala

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			20					25					30		
Gln	Val	Ser	Ser	Asp	Val	Asp	Glu	Gln	Leu	Ser	Lys	Ser	Val	Lys	Asp
		35					40					45			
Lys	Val	Leu	Leu	Pro	Cys	Arg	Tyr	Asn	Ser	Pro	His	Glu	Asp	Glu	Ser
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Glu	Asp	Arg	Ile	Tyr	Trp	Gln	Lys	His	Asp	Lys	Val	Val	Leu	Ser	Val
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Ile	Ala	Gly	Lys	Leu	Lys	Val	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Leu
				85					90					95	
Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile	Ile	Leu	Gly	Leu	Val	Leu	Ser
			100					105					110		
Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg	Gly	Thr
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Tyr	Glu	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys	Ala	Asp
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Phe	Ser	Thr	Pro	Asn	Ile	Thr	Glu	Ser	Gly	Asn	Pro	Ser	Ala	Asp	Thr
145					150					155					160
Lys	Arg	Ile	Thr	Cys	Phe	Ala	Ser	Gly	Gly	Phe	Pro	Lys	Pro	Arg	Phe
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Ser	Trp	Leu	Glu	Asn	Gly	Arg	Glu	Leu	Pro	Gly	Ile	Asn	Thr	Thr	Ile
			180					185					190		
Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	Tyr	Thr	Ile	Ser	Ser	Gln	Leu	Asp
		195					200					205			
Phe	Asn	Thr	Thr	Arg	Asn	His	Thr	Ile	Lys	Cys	Leu	Ile	Lys	Tyr	Gly
	210					215					220				

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
260 265 270

Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
275 280 285

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
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Phe Leu
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<213> Artificial sequence

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Cys Val Val Leu Ala Phe Ser Thr Pro Ile Ser Arg Thr Cys Gly Pro
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Pro Trp Asn Ile Thr Thr Val Asn Val Val Val Phe Arg Ser Thr Gly
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Pro Glu Thr
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1 5 10 15

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Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

gtg gag ctc agc tgc gct tgc cct gaa gga agc cgt ttt gat tta aat 144
Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

gat gtt tac gta tat tgg caa acc agt gag tcg aaa acc gtg gtg acc 192
Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

tac cac atc cca cag aac agc tcc ttg gaa aac gtg gac agc cgc tac 240
Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

cgg aac cga gcc ctg atg tca ccg gcc ggc atg ctg cgg ggc gac ttc 288
Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

tcc ctg cgc ttg ttc aac gtc acc ccc cag gac gag cag aag ttt cac 336
Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

tgc ctg gtg ttg agc caa tcc ctg gga ttc cag gag gtt ttg agc gtt 384
Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

gag gtt aca ctg cat gtg gca gca aac ttc agc gtg ccc gtc gtc agc 432
Glu Val Thr Leu His Val Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

gcc ccc cac agc ccc tcc cag gat gag ctc acc ttc acg tgt aca tcc 480
Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

ata aac ggc tac ccc agg ccc aac gtg tac tgg atc aat aag acg gac 528
Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

aac agc ctg ctg gac cag gct ctg cag aat gac acc gtc ttc ttg aac 576
Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

atg cgg ggc ttg tat gac gtg gtc agc gtg ctg agg atc gca cgg acc 624
Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

ccc agc gtg aac att ggc tgc tgc ata gag aac gtg ctt ctg cag cag 672
Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

aac ctg act gtc ggc agc cag aca gga aat gac atc gga gag aga gac 720
Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

aag atc aca gag aat cca gtc agt acc ggc gag aaa aac gcg gcc acg 768
Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

tgg agc atc ctg gct gtc ctg tgc ctg ctt gtg gtc gtg gcg gtg gcc	816
Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala	
260 265 270	
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275 280 285	
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<213> Homo sapiens	
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35 40 45	
Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr	
50 55 60	
Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr	
65 70 75 80	
Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe	
85 90 95	
Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His	
100 105 110	
Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val	
115 120 125	
Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser	
130 135 140	
Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser	
145 150 155 160	
Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp	
165 170 175	
Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn	
180 185 190	

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

<210> 13
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<212> PRT
<213> Homo sapiens

<400> 13

Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp Val Glu Leu Ser Cys
1 5 10 15

Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr
20 25 30

Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr Tyr His Ile Pro Gln
35 40 45

Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu
50 55 60

Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe
65 70 75 80

Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu Val Leu Ser
85 90 95

Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val Thr Leu His
100 105 110

Val Ala Ala Asn Phe Ser Val Pro Val Val Ser Ala Pro His Ser Pro
115 120 125

Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser Ile Asn Gly Tyr Pro
130 135 140

Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp Asn Ser Leu Leu Asp
145 150 155 160

Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn Met Arg Gly Leu Tyr
165 170 175

Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr Pro Ser Val Asn Ile
180 185 190

Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln Asn Leu Thr Val Gly
195 200 205

Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile Thr Glu Asn
210 215 220

Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr Trp Ser Ile Leu Ala
225 230 235 240

Val Leu Cys Leu Leu Val Val Val Ala Val Ala Ile Gly Trp Val Cys
245 250 255

Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
260 265

<210> 14
<211> 276
<212> PRT
<213> Mus musculus

<400> 14

Glu Thr Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys
1 5 10 15

Ile Asp Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr
20 25 30

Trp Gln Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr
35 40 45

Lys Ser Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His
50 55 60

Leu Ser Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys
65 70 75 80

Asn	Val	Thr	Pro	Gln	Asp	Thr	Gln	Glu	Phe	Thr	Cys	Arg	Val	Phe	Met
				85					90					95	
Asn	Thr	Ala	Thr	Glu	Leu	Val	Lys	Ile	Leu	Glu	Glu	Val	Val	Arg	Leu
			100					105					110		
Arg	Val	Ala	Ala	Asn	Phe	Ser	Thr	Pro	Val	Ile	Ser	Thr	Ser	Asp	Ser
		115					120					125			
Ser	Asn	Pro	Gly	Gln	Glu	Arg	Thr	Tyr	Thr	Cys	Met	Ser	Lys	Asn	Gly
	130					135					140				
Tyr	Pro	Glu	Pro	Asn	Leu	Tyr	Trp	Ile	Asn	Thr	Thr	Asp	Asn	Ser	Leu
145					150					155					160
Ile	Asp	Thr	Ala	Leu	Gln	Asn	Asn	Thr	Val	Tyr	Leu	Asn	Lys	Leu	Gly
				165					170					175	
Leu	Tyr	Asp	Val	Ile	Ser	Thr	Leu	Arg	Leu	Pro	Trp	Thr	Ser	Arg	Gly
			180					185					190		
Asp	Val	Leu	Cys	Cys	Val	Glu	Asn	Val	Ala	Leu	His	Gln	Asn	Ile	Thr
		195					200					205			
Ser	Ile	Ser	Gln	Ala	Glu	Ser	Phe	Thr	Gly	Asn	Asn	Thr	Lys	Asn	Pro
	210					215					220				
Gln	Glu	Thr	His	Asn	Asn	Glu	Leu	Lys	Val	Leu	Val	Pro	Val	Leu	Ala
225					230					235					240
Val	Leu	Ala	Ala	Ala	Ala	Phe	Val	Ser	Phe	Ile	Ile	Tyr	Arg	Arg	Thr
				245					250					255	
Arg	Pro	His	Arg	Ser	Tyr	Thr	Gly	Pro	Lys	Thr	Val	Gln	Leu	Glu	Leu
			260					265					270		
Thr	Asp	His	Ala												
		275													
<210>	15														
<211>	125														
<212>	PRT														
<213>	Artificial sequence														
<220>															
<223>	Synthetic														
<400>	15														
Glu	Glu	Val	Ala	Met	Val	Gly	Ser	Val	Leu	Ser	Cys	Pro	Phe	Leu	Tyr
1				5					10					15	

Val Tyr Trp Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg
20 25 30

Ser Met Gly Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys
35 40 45

Val Leu Val Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr
50 55 60

Thr Cys Ser Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn
65 70 75 80

Ser Leu Asp Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val
85 90 95

Ser Leu Arg Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly
100 105 110

Lys Lys Leu Ala Val Leu Val Ile Arg Arg Ser Tyr Gly
115 120 125

<210> 16
<211> 1294
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(199)
<223>

<220>
<221> CDS
<222> (200)..(1105)
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<400> 16
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cgtccgcggg agcgcagtta gagccgatct cccgcgcccc gaggttgctc ctctccgagg 120
tctcccgcgg cccaagttct ccgcgccccg aggtctccgc gccccgaggt ctccgcggcc 180
cgaggtctcc gcccgcacc atg cgg ctg ggc agt cct gga ctg ctc ttc ctg 232
Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu
1 5 10
ctc ttc agc agc ctt cga gct gat act cag gag aag gaa gtc aga gcg 280
Leu Phe Ser Ser Leu Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala
15 20 25
atg gta ggc agc gac gtg gag ctc agc tgc gct tgc cct gaa gga agc 328
Met Val Gly Ser Asp Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser
30 35 40

cgt Arg	ttt Phe 45	gat Asp	tta Leu	aat Asn	gat Asp	gtt Val 50	tac Tyr	gta Val	tat Tyr	tgg Trp	caa Gln 55	acc Thr	agt Ser	gag Glu	tcg Ser	376
aaa Lys 60	acc Thr	gtg Val	gtg Val	acc Thr	tac Tyr 65	cac His	atc Ile	cca Pro	cag Gln	aac Asn 70	agc Ser	tcc Ser	ttg Leu	gaa Glu	aac Asn 75	424
gtg Val	gac Asp	agc Ser	cgc Arg	tac Tyr 80	cgg Arg	aac Asn	cga Arg	gcc Ala	ctg Leu 85	atg Met	tca Ser	ccg Pro	gcc Ala	ggc Gly 90	atg Met	472
ctg Leu	cgg Arg	ggc Gly	gac Asp 95	ttc Phe	tcc Ser	ctg Leu	cgc Arg	ttg Leu 100	ttc Phe	aac Asn	gtc Val	acc Thr	ccc Pro 105	cag Gln	gac Asp	520
gag Glu	cag Gln	aag Lys 110	ttt Phe	cac His	tgc Cys	ctg Leu 115	gtg Val	ttg Leu	agc Ser	caa Gln	tcc Ser	ctg Leu 120	gga Gly	ttc Phe	cag Gln	568
gag Glu 125	gtt Val	ttg Leu	agc Ser	gtt Val	gag Glu 130	gtt Val	aca Thr	ctg Leu	cat His	gtg Val	gca Ala 135	gca Ala	aac Asn	ttc Phe	agc Ser	616
gtg Val 140	ccc Pro	gtc Val	gtc Val	agc Ser	gcc Ala 145	ccc Pro	cac His	agc Ser	ccc Pro	tcc Ser 150	cag Gln	gat Asp	gag Glu	ctc Leu	acc Thr 155	664
ttc Phe	acg Thr	tgt Cys	aca Thr	tcc Ser 160	ata Ile	aac Asn	ggc Gly	tac Tyr	ccc Pro 165	agg Arg	ccc Pro	aac Asn	gtg Val	tac Tyr 170	tgg Trp	712
atc Ile	aat Asn	aag Lys	acg Thr 175	gac Asp	aac Asn	agc Ser	ctg Leu 180	ctg Leu	gac Asp	cag Gln	gct Ala	ctg Leu	cag Gln	aat Asn	gac Asp	760
acc Thr	gtc Val	ttc Phe 190	ttg Leu	aac Asn	atg Met	cgg Arg	ggc Gly 195	ttg Leu	tat Tyr	gac Asp	gtg Val	gtc Val	agc Ser	gtg Val	ctg Leu	808
agg Arg 205	atc Ile	gca Ala	cgg Arg	acc Thr	ccc Pro	agc Ser 210	gtg Val	aac Asn	att Ile	ggc Gly	tgc Cys 215	tgc Cys	ata Ile	gag Glu	aac Asn	856
gtg Val 220	ctt Leu	ctg Leu	cag Gln	cag Gln	aac Asn 225	ctg Leu	act Thr	gtc Val	ggc Gly	agc Ser 230	cag Gln	aca Thr	gga Gly	aat Asn	gac Asp 235	904
atc Ile	gga Gly	gag Glu	aga Arg	gac Asp 240	aag Lys	atc Ile	aca Thr	gag Glu	aat Asn 245	cca Pro	gtc Val	agt Ser	acc Thr	ggc Gly 250	gag Glu	952
aaa Lys	aac Asn	gcg Ala 255	gcc Ala	acg Thr	tgg Trp	agc Ser	atc Ile 260	ctg Leu	gct Ala	gtc Val	ctg Leu	tgc Cys 265	ctg Leu	ctt Leu	gtg Val	1000
gtc Val	gtg Val	gcg Ala 270	gtg Val	gcc Ala	ata Ile	ggc Gly	tgg Trp 275	gtg Val	tgc Cys	agg Arg	gac Asp	cga Arg	tgc Cys	ctc Leu	caa Gln	1048
cac His 285	agc Ser	tat Tyr	gca Ala	ggt Gly	gcc Ala	tgg Trp 290	gct Ala	gtg Val	agt Ser	ccg Pro	gag Glu 295	aca Thr	gag Glu	ctc Leu	act Thr	1096

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ggc cac gtt tgaccggagc tcaccgcca gagcgtggac agggcttccg      1145
Gly His Val
300

tgagacgcca ccgtgagagg ccaggtggca gcttgagcat ggactcccag actgcagggg      1205
agcacttggg gcagccccca gaaggaccac tgctggatcc cagggagaac ctgctggcgt      1265
tggctgtgat cctggaatga ggccctttc      1294

<210> 17
<211> 302
<212> PRT
<213> Homo sapiens

<400> 17

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1          5          10          15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
          20          25          30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
          35          40          45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
          50          55          60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65          70          75          80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
          85          90          95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
          100          105          110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
          115          120          125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130          135          140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145          150          155          160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
          165          170          175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
          180          185          190

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Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 18
<211> 302
<212> PRT
<213> Homo sapiens

<400> 18

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 19
<211> 322
<212> PRT
<213> Mus musculus

<400> 19

Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
1 5 10 15

Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30

Leu Phe Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
305 310 315 320

His Ala

<210> 20
<211> 143
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 20

Met Leu Pro Gly Leu Leu Phe Leu Leu Ser Ser Leu Ala Glu Glu Val
1 5 10 15

Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr Val Tyr Trp
20 25 30

Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg Ser Met Gly
35 40 45

Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys Val Leu Val
50 55 60

Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr Thr Cys Ser
65 70 75 80

Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn Ser Leu Asp
85 90 95

Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val Ser Leu Arg
100 105 110

Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly Lys Lys Leu
115 120 125

Ala Val Leu Val Ile Arg Arg Ser Tyr Gly Val Glu Leu Thr His
130 135 140

<210> 21
<211> 1370
<212> DNA
<213> Homo sapiens

<220>

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<221> 5'UTR
<222> (1)..(165)
<223>

<220>
<221> CDS
<222> (166)..(762)
<223>

<400> 21
aacaatttca cacaggaaac agctatgacc atgattacgc caagctctaa tacgactcac      60
tatagggaaa gctggtacgc ctgcagggtac cgggtccggaa ttcccggggtc gacccacgcg      120
tccgtgaaca ctgaacgcga ggactgttaa ctgtttctgg caaac atg aag tca ggc      177
                                     Met Lys Ser Gly
                                     1

ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga      225
Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly
5                               10                               15                               20

gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt cac aac gga      273
Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
                               25                               30                               35

ggg gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa      321
Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
                               40                               45                               50

atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca      369
Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
                               55                               60                               65

aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat      417
Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
70                               75                               80

tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac      465
Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
85                               90                               95                               100

cat tct cat gcc aac tat tac ttc tgc aac cta tca att ttt gat cct      513
His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
                               105                               110                               115

cct cct ttt aaa gta act ctt aca gga gga tat ttg cat att tat gaa      561
Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu
                               120                               125                               130

tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata gga tgt gca      609
Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala
                               135                               140                               145

gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att tgt tgg ctt      657
Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu
                               150                               155                               160

aca aaa aag aag tat tca tcc agt gtg cac gac cct aac ggt gaa tac      705
Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
165                               170                               175                               180

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atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc aca gat 753
Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
185 190 195

gtg acc cta taatatggaa ctctggcacc caggcatgaa gcacgttggc 802
Val Thr Leu

cagttttcct caacttgaag tgcaagattc tcttatttcc gggaccacgg agagtctgac 862

ttaactacat acatcttctg ctggtgtttt gttcaatctg gaagaatgac tgtatcagtc 922

aatggggatt ttaacagact gccttggtac tgccgagtcc tctcaaaaca aacaccctct 982

tgcaaccagc tttggagaaa gccagctcc tgtgtgctca ctgggagtgg aatccctgtc 1042

tccacatctg ctctagcag tgcacagcc agtaaaacaa acacatttac aagaaaaatg 1102

ttttaaagat gccaggggta ctgaatctgc aaagcaaatg agcagccaag gaccagcatc 1162

tgtccgcatt tcactatcat actacctctt ctttctgtag ggatgagaat tcctctttta 1222

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ctgtacatta gtacatactc agtactctcc ttcaattgct gaaccccagt tgaccatttt 1342

accaagactt tagatgcttt cttgtgcc 1370

<210> 22
<211> 199
<212> PRT
<213> Homo sapiens

<400> 22

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 23
<211> 199
<212> PRT
<213> Homo sapiens

<400> 23

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 24
<211> 200
<212> PRT
<213> Mus musculus

<400> 24

Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
1 5 10 15

Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
20 25 30

Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 25
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 25
accatgcggc tgggcagtc tggg 24

<210> 26
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 26
tgggtgacctt ccacatccca cag 23

<210> 27
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oglionucleotide

<400> 27
tccgatgtca tttcctgtct ggc 23

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